

1. (Currently Amended) A method of identifying one or more nucleic acid sequences useful as a biomarker for a disease to be detected, comprising:
 - (a) identifying one or more nucleic acid sequences that are down-regulated in a diseased ~~cells~~ cell compared to ~~normal-cells~~ a control cell, wherein the nucleic acid sequences comprise at least one methylated CpG site in a promoter-first exon region;
 - (b) comparing an expression level of the nucleic acid sequences from (a) with an expression level of the nucleic acid sequences from (a) that have been demethylated; and
 - (c) identifying those nucleic acid sequences exhibiting a significant increase in the expression level after demethylation treatment as compared to the expression level of the same nucleic acid sequences in the methylated state; wherein those nucleic acid sequences exhibiting a significant increase in the expression level after demethylation treatment are useful as a biomarker for a disease to be detected and wherein the disease is cancer.
2. (Canceled)
3. The method of claim 1, wherein the promoter-first exon region spans about 1000 base pairs upstream of the first exon and about 1000 base pairs downstream of the first exon.
4. - 27. (Canceled)
28. (New) The method of claim 1 wherein the diseased cell comprises a cell from colon and/or rectal tissue.
29. (New) The method of claim 28 wherein the one or more nucleic acid sequences that are down-regulated in a diseased cell are down-regulated at least about 2 fold, at least about 5 fold, at least about 20 fold, or at least about 50 fold as compared to the control cell.
30. (New) The method of claim 29 wherein the disease is colon or colorectal cancer.